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13. ABSTRACT (Maximum 200 words) Our laboratory is studying the polyurethanase enzymes and genes that encode them from three species of <i>Pseudomonas</i> . We have purified and characterized five polyurethane hydrolyzing proteins and cloned four polyurethanase genes, in which two have been sequenced. Nucleotide sequencing of the polyurethanase genes revealed that the deduced polypeptide sequence contains a serine-hydrolase consensus sequence GX SXG. The polypeptides lacked an N-terminal signal peptide, but did contain a short region toward the C-terminus that has been observed in secreted lipases. The most closely related proteins to the polyurethanases had amino acid sequences homologies of 70% for four lipases from <i>P. fluorescens</i> and 51% for lipases from <i>Serratia marcescens</i> . Northern blot analysis revealed that the polyurethanase genes are constitutively expressed. The results obtained from this study has yielded valuable information that is essential for an understanding of the biochemical and genetic properties of bacterial polyurethanases and how these properties may be utilized to improve polyurethane degradation. The study has a potentially major impact on understanding mechanisms by which enzymes degrade polyurethane.				
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GRANT TITLE: Molecular Characterization of Polyurethanase Genes and Proteins from *Pseudomonas*

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OBJECTIVE: To elucidate the enzymology and mechanism of polyurethane degradation in *Pseudomonas fluorescens*, *Pseudomonas chlororaphis*, and *Comamonas acidovorans*.

APPROACH: Polyurethanase proteins are purified and characterized from the various pseudomonads of interest. The purified enzymes are N-terminal sequenced and degenerate oligo-nucleotides are synthesized. The oligo-nucleotides are used to probe genomic libraries of the various pseudomonads in which to corresponding genes can be identified. The cloned polyurethanase genes are analyzed by DNA sequencing, RNA analysis, and expression in *E. coli*.

ACCOMPLISHMENTS:

Our laboratory is currently studying the polyurethanase enzymes and genes that encode them from three species of *Pseudomonas* (Table 1). Interestingly, the three species of bacteria produce different polyurethanase activities but are inhibited by serine hydrolase inhibitors. These data suggest that either esterase and/or protease activities are involved in the degradation of Impranil.

TABLE 1. Characteristics of Purified PUase Isolated by our Laboratory.

Bacterial Isolate	Molecular Mass	Enzyme Specificity	Inhibition	Heat Stable ¹
<i>P. fluorescens</i>	29 kDa	Protease	PMSF	+
<i>P. fluorescens</i>	48 kDa ^{2,3}	Esterase	PMSF	-
<i>P. chlororaphis</i>	63 kDa ^{2,3}	Esterase/Protease	PMSF	+
<i>P. chlororaphis</i>	31 kDa	Esterase	PMSF	+
<i>P. chlororaphis</i>	70 kDa ²	Esterase	PMSF	-
<i>C. acidovorans</i>	42 kDa	Esterase/Protease	PMSF/TI	+

¹Enzyme activity (100%) after 10 min at 100°C

²Enzyme has been cloned and expressed in *E. coli*

³Gene has been sequenced

Growth of *Comamonas acidovorans* on polyurethane resulted in obtaining growth parameters of K_s and μ_{max} values of $0.3 \text{ mg} \cdot \text{ml}^{-1}$ and $0.7 \text{ doublings} \cdot \text{h}^{-1}$ respectively (Allen *et al.*, 1999). Our laboratory has purified and characterized a 42kDa PUase enzyme displaying esterase/protease activity (Allen *et al.*, 1999). Nakajima-Kambe *et al.* (1995, 1997) reported a strain of *Comamonas acidovorans* that could utilize solid polyester PU as the sole carbon and nitrogen source. These authors indicated the role of an extracellular membrane bound esterase

activity in PU degradation. Purification of the membrane bound esterase revealed a thermally labile protein having a 62 kDa molecular mass (Akutsu *et al.*, 1998).

Growth of *Pseudomonas chlororaphis* on polyurethane resulted in obtaining growth parameters of K_s and μ_{max} values of $0.9 \text{ mg}\cdot\text{ml}^{-1}$ and $1.3 \text{ doublings}\cdot\text{h}^{-1}$ respectfully (Ruiz *et al.*, 1999). Two PUase enzymes have been purified and characterized, a 65 kDa esterase/protease and a 31 kDa esterase (Ruiz *et al.*, 1999). In addition to the enzymology, a PUase gene encoding a 63 kDa protein has been cloned in *E. coli*. The gene encoding the 63 kDa PUase, *pueA*, has been expressed and sequenced (Genebank, Accession AF069748). An open reading frame (ORF), 1,854 nucleotides in length, was observed in the cloned insert by codon analysis, starting with an AUG codon in nucleotide 175 and stopping with an UGA codon in nucleotide 2,029. Identity searching in database with the BLAST program indicated a strong similarity of this ORF to several lipase genes. Therefore, the sequenced gene was called *pueA* (polyurethanase-esterase A). The initiating AUG codon was preceded 7 nucleotides by a plausible ribosomal binding site with an AAGAGG. The deduced protein PueA has 617 amino acid residues and a molecular mass of 65 kDa. The encoded amino acid sequence of PueA was aligned with six other extracellular lipases from *Pseudomonas fluorescens* and *Serratia marcescens*. The PueA amino acid sequence showed a high identity with these lipases (ranging from 58 to 75%). Two highly conserved regions were observed for PueA and the extracellular lipases (Figure 1). A putative catalytic domain for serine hydrolases, amino acids 203-211, was observed. The sequence motif, G-H-S-L-G, as well as the location were conserved among all seven polypeptides. In addition, a second conserved region was observed for PueA and the six lipases. A common motif among secreted lipases was observed at amino acids 364 to 400. The secretion sequence motif, G-G-X-G-X-D-X-X-E was conserved as well as the location. Interestingly, the location of the secretion motif is consistently 163 amino acid residues downstream from the putative catalytic motif for each of the seven polypeptides. The size of the *pueA* mRNA was determined by Northern blot analysis. A 1900 nucleotide transcript was detected from *P. chlororaphis* grown in various carbon sources. The transcript analysis indicates that the *pueA* gene is constitutively expressed. The gene encoding the 31kDa protein has not been isolated, however the *P. chlororaphis* library generated is currently being screened for its presence.

Growth of *Pseudomonas fluorescens* on polyurethane resulted in obtaining growth parameters of K_s and μ_{max} values of $0.9 \text{ mg}\cdot\text{ml}^{-1}$ and $1.6 \text{ doublings}\cdot\text{h}^{-1}$ respectfully (Howard and Blake, 1999). Two PUase enzymes have been purified and characterized from this bacterial isolate, a 29kDa protease (Howard and Blake, 1999) and a 48kDa esterase (Vega *et al.*, 1999). In addition, to the enzymology of the PUases the gene encoding a 48 kDa protein has been cloned and expressed in *E. coli* (Vega *et al.*, 1999). The gene encoding *PulA* has been sequenced (GeneBank AF144089). The deduced amino acid sequence has 461 amino acid residues and a molecular mass of 49 kDa. The *PulA* amino acid sequence showed high identity with the six lipases (58 to 75%) and PueA from *P. chlororaphis* (85%). The size of the *pulA* mRNA was determined by Northern blot analysis. A 1500 nucleotide transcript was detected from *P. fluorescens* grown in various carbon sources. The transcript analysis indicates that the *pulA* gene is constitutively expressed. The gene encoding for the 29kDa protease has not been isolated, however the *P. fluorescens* library generated is currently being screened for its presence.

Figure 1. Comparison of putative active sites and secretion sites for the PueA from *P. chlororaphis* and six extracellular lipases. The numbers indicate the position of the amino acid residues within the protein sequence. Percent identity of complete gene when compared to PueA is indicated. Panel A, Active site region with identical residues boxed. Panel B, Secretion signal region with identical residues shaded.

		Active Site										% Identity	
<i>Pseudomonas fluorescens</i> SIK W1	202-	Val	Ser	Gly	His	Ser	Leu	Gly	Gly	Leu		-210	58
<i>Pseudomonas fluorescens</i> B52	203-	Val	Ser	Gly	His	Ser	Leu	Gly	Gly	Leu		-211	70
<i>Pseudomonas</i> LS107d2	203-	Val	Ser	Gly	His	Ser	Leu	Gly	Gly	Leu		-211	67
<i>Serratia marcescens</i> SM6	203-	Val	Ser	Gly	His	Ser	Leu	Gly	Gly	Leu		-211	61
<i>Serratia marcescens</i> Sr41	202-	Ile	Ser	Gly	His	Ser	Leu	Gly	Gly	Leu		-210	61
<i>Pseudomonas chlororaphis</i>	203-	Val	Ser	Gly	His	Ser	Leu	Gly	Gly	Leu		-211	-
<i>Pseudomonas fluorescens</i>	180-	Val	Ser	Gly	His	Ser	Leu	Gly	Gly	Met		-188	85

B

<i>Serratia marcescens</i> SM6	364-	E	T	H	S	G	P	T	F	I	G	S	D	G	N	D	L	I	K	G	G	K	G	N	D	Y	L	E	G	R	D	G	D	I	F	R	-400	
<i>Serratia marcescens</i> Sr41	363-	E	T	H	S	G	P	T	F	I	G	S	D	G	N	D	L	I	K	G	G	K	G	N	D	Y	L	E	G	R	D	G	D	I	F	R	-399	
<i>Pseudomonas fluorescens</i> SIK W1	363-	E	P	H	T	G	N	T	F	I	G	S	D	G	N	D	L	I	Q	G	G	K	G	A	D	F	I	E	G	G	K	G	N	D	T	I	R	-399
<i>Pseudomonas fluorescens</i> B52	363-	E	P	H	K	G	N	T	F	I	G	S	D	G	N	D	L	I	Q	G	G	N	G	A	D	F	I	E	G	G	K	G	N	D	T	I	R	-399
<i>Pseudomonas</i> LS107d2	363-	E	P	H	K	G	D	T	F	I	G	S	A	G	N	D	L	I	Q	G	G	K	G	A	D	F	I	E	A	A	K	G	N	D	T	I	R	-399
<i>Pseudomonas chlororaphis</i>	364-	E	T	H	K	G	S	T	F	I	G	S	D	G	N	D	L	I	Q	G	G	S	G	N	D	Y	L	E	G	G	A	G	N	D	T	F	R	-400
<i>Pseudomonas fluorescens</i>	340-	E	A	H	K	G	N	T	F	I	G	S	D	G	D	D	L	I	K	G	G	R	G	A	D	F	I	E	G	G	K	G	N	D	T	I	P	-376
Consensus Sequence		G G X G X D X X X																																				

SIGNIFICANCE:

The goal of the proposed research is to dissect the polyurethanase enzymes using an integrated enzymologic and genetic approach. The proposed study will involve appropriate and innovative strategies for studying each of the single enzymes and genes involved in the degradation of polyurethane. The genes and gene products responsible for the degradation of polyurethane can then be identified and characterized biochemically and genetically. Thus, the proposed studies should culminate in development of a model system in which the role of single genes and gene products in polyurethane degradation can be assessed. The results obtained from this study will yield valuable information that is essential for an understanding of the biochemical and genetic properties of bacterial polyurethanase and how these properties may be utilized to improve polyurethane degradation. More specifically, characterization of the enzymology of polyurethanases will be instrumental to understanding the mechanism involved in polyurethane degradation by bacteria. A more efficient degradation of polyurethane waste biomass will provide a major contribution to both the environment and the consumer.

The long term goals of this research is to initiate a program aimed at a better understanding of the mechanism of polyurethane degradation by bacteria. One approach is to study each enzyme and gene at the single gene level using an integrated enzymological, biochemical, physical, and genetic program. **The proposed studies should culminate in development of a novel anaerobic model system in which the role of single genes and gene products in polyurethane degradation can be assessed, and the degradation products established.**

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